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Transcriptome Analysis of Saffron (crocus sativus L.) Stigma Focusing on Identification Genes Involved in the Biosynthesis of Crocin

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Abstract : Saffron (Crocus sativus L.) is one of the most important spice and medicinal plants. The three-branch style of C. sativus flowers are the most important economic part of the plant and known as saffron, which has several medicinal properties. Despite the economic and biological significance of this plant, knowledge about its molecular characteristics is very limited. In the present study, we, for the first time, constructed a comprehensive dataset for C. sativus stigma through de novo transcriptome sequencing. We performed de novo transcriptome sequencing of C. sativus stigma using the Illumina paired-end sequencing technology. A total of 52075128 reads were generated and assembled into 118075 unigenes, with an average length of 629 bp and an N50 of 951 bp. A total of 66171unigenes were identified, among them, 66171 (56%) were annotated in the non-redundant National Center for Biotechnology Information (NCBI) database, 30938 (26%) were annotated in the Swiss-Prot database, 10273 (8.7%) unigenes were mapped to 141 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway database, while 52560 (44%) and 40756 (34%) unigenes were assigned to Gen Ontology (GO) categories and Eukaryotic Orthologous Groups of proteins (KOG), respectively. In addition, 65 candidate genes involved in three stages of crocin biosynthesis were identified. Finally, transcriptome sequencing of saffron stigma was used to identify 6779 potential microsatellites (SSRs) molecular markers. High-throughput de novo transcriptome sequencing provided a valuable resource of transcript sequences of C. sativus in public databases. In addition, most of candidate genes potentially involved in crocin biosynthesis were identified which could be further utilized in functional genomics studies. Furthermore, numerous obtained SSRs might contribute to address open questions about the origin of this amphiploid spices with probable little genetic diversity.

Keywords : saffron, transcriptome, NGS, bioinformatic
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